

Genware version 4.5
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OM protein - protein search, using sw model

Run on: March 12, 2002, 12:49:01 : Search time 22.94 seconds
(without alignments)
43,206 Million cell updates/sec

Title: US-09-801-784-36
Perfect score: 50
Sequence: 1 PSVAVALYSP 10

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 68
Listing first 45 summaries

Database: PIR_68*

1: pirt1*
2: pirt2*
3: pirt3*
4: pirt4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	88.0	171	2	A41467
2	40	80.0	170	1	YOEBC1
3	40	80.0	170	1	R56617
4	38	76.0	2344	2	S64740
5	36	72.0	234	2	S22134
6	36	72.0	326	2	S27901
7	36	72.0	326	2	T17743
8	36	72.0	377	1	MCN2P2
9	36	72.0	427	2	T41257
10	35	70.0	537	2	S62749
11	35	70.0	251	2	A55523
12	35	70.0	260	2	S72748
13	35	70.0	374	1	DEHUAS
14	35	70.0	424	1	A56436
15	35	70.0	424	2	T34663
16	35	70.0	444	2	S64912
17	35	70.0	486	2	S74319
18	35	70.0	804	2	H75549
19	35	70.0	963	2	S45167
20	35	70.0	2344	2	S55399
21	34	68.0	331	2	G75035
22	34	68.0	331	2	T40466
23	34	68.0	460	2	R82549
24	34	68.0	540	1	OYHDCR
25	34	68.0	570	2	T37314
26	34	68.0	610	2	T35797
27	34	68.0	1877	2	T40550
28	34	68.0	2016	2	A48195
29	33	66.0	115	2	S75392

36	33	66.0	156	2	CR2971
37	33	66.0	161	2	T52406
38	33	66.0	169	2	T52410
39	33	66.0	201	2	T52408
40	33	66.0	212	2	T01605
41	33	66.0	225	2	H75548
42	33	66.0	310	2	T43158
43	33	66.0	314	2	T43299
44	33	66.0	375	1	MFNZ41
45	33	66.0	409	2	E70643
46	33	66.0	441	2	S54734
47	33	66.0	547	1	PKADP4
48	33	66.0	563	1	T46845
49	33	66.0	664	1	H32243

ALIGNMENTS

495011 1
A41467
Luminal protein csaA - Escherichia coli plasmid pEU405
N:Alternate names: CSI plus major subunit
C:Species: Escherichia coli
C:Date: 30-Jun-1992 *Sequence revision 30-Jun-1992 *Text change 21 Aug 1992
C:Accession: A14467: S19003
R:Peretz-Gasal, J.; Shattley, J.S.; Stroth, J.R.
Infect. Immun. 58: 3594-3603, 1990
A:Title: Gene encoding the major subunit of CSI plus of human enterococcal strain Escherichia coli
A:Reference number: A14467: MIMD:9104170
A:Accession: A14467
A:Molecule type: DNA
A:Residues: 1-171 - JOR
A:Cross-reference: EMBL: X62879; NID:041169; PIRN: P04467; J. H. 941-171
C:Genetics:
A:Gene: csaA
A:Genome: Plasmid
C:Superfamily: csaA luminal protein
Query Match 88.0% Score 44 DB 2: (month 11)
Host local similarity 80.0% Pred. No. 0.245
Matches 8: Conservative 2: Mismatches 0: Gaps 0
CY 1 PSVAVALYSP 10
LB 49 PSVAVALYSP 58
RESULT 2
csaA luminal protein precursor - Escherichia coli
N:Alternate names: csaA plasmid colonization factor and (csaA)
C:Species: Escherichia coli
C:Date: 14-Nov-1983 *Sequence revision 30-Jun-1991 *Text change 15 Nov 1996
C:Accession: A05899: A03495; A43441
R:Kajalaidon, T.R.; Evans, D.J.; So, M.; Lee, C.H.
Infect. Immun. 57: 1126-1136, 1989
A:Title: Molecular cloning and nucleotide sequence of the cloned csaA gene
A:Reference number: A05899: MIMD:85174309
A:Accession: A05899
A:Molecule type: DNA

S27901
 Site-specific DNA-methyltransferase (adenine-specific) (EC 2.1.1.72) (VIAI) Chloroella
 N:Alternate names: DNA adenine methyltransferase (VIAI)
 C:Species: Chloroella virus PhCV-1
 C:Date: 09-Jun-1994 #sequence_revision 10 Nov-1995 #text_change 05-May-2006
 C:Accession: S55442; S27901
 R:Zhang, Y.; Nelson, M.; Nietfeldt, J.W.; Huibank, B.E.; van Etten, J.L.
 Nucleic Acids Res. 20, 5151-5156, 1992
 A:Title: Characterization of chloroella virus PhCV-1 (VIAI) restriction and modification
 A:Reference number: S55442; M01D:93065201
 A:Accession: S55442
 A:Molecule type: DNA
 A:Residues: 1-326 SEITs
 A:Cross-references: EMBL:M86349; NID:9323316; PID:9323317
 C:Superfamily: site-specific methyltransferase (adenine-specific) NID11
 C:Keywords: methyltransferase; S-adenosylmethionine

Query Match 72.0%; Score 36; DB 2; Length 326;
 Best Local Similarity 70.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 PSAAVITVSP 10
 1 11111
 DB 95 PGFVITVSP 104

RESULT 7
 11743
 Site-specific DNA-methyltransferase (adenine-specific) (EC 2.1.1.72) - Chloroella virus 1
 C:Species: Chloroella virus PhCV-1
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-May-2006
 C:Accession: T17743
 R:Graves, M.V.; Van Etten, J.L.
 Submitted to the EMBL Data Library: May 1999
 A:Reference number: Z18806
 A:Accession: T17743
 A:Status: preliminary; translated from GH/EMBL/M084
 A:Molecule type: DNA
 A:Residues: 1-326 <GBA>
 A:Cross-references: EMBL:042580; NID:94028896; PID:AA096619.1
 C:Genetics:
 A:Note: A251R
 C:Superfamily: site-specific methyltransferase (adenine-specific) NID11
 C:Keywords: methyltransferase; S-adenosylmethionine

Query Match 72.0%; Score 36; DB 2; Length 326;
 Best Local Similarity 70.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 PSAAVITVSP 10
 1 11111
 DB 95 PGFVITVSP 104

RESULT 8
 MENT2
 Matrix protein - parainfluenza virus type 2
 C:Species: Parainfluenza virus type 2
 C:Date: 31-Mar-1992 #sequence_revision 01-Mar-1992 #text_change 16-Jul-1999
 C:Accession: A56421; S16661
 R:Kawano, M.; Bando, H.; Ohmoto, S.; Okamoto, K.; Kondo, K.; Isumidomo, M.; Nishio, M.
 Virology 179, 857-861, 1990
 A:Title: Complete nucleotide sequence of the matrix gene of human parainfluenza type 2
 A:Reference number: A56421; M01D:91034954
 A:Accession: A56421
 A:Molecule type: genomic RNA
 A:Residues: 1-377 <KAM>
 A:Cross-references: GH:M62744; NID:9332730; PID:AAA6862.1; PID:9332731;
 R:Kawano, M.; Okamoto, K.; Bando, H.; Kondo, K.; Isumidomo, M.; Kumada, H.; Nishio, M.;
 Nucleic Acids Res. 19, 2739-2746, 1991
 A:Title: Characterizations of the human parainfluenza type 2 virus gene encoding the E

A:Reference number: S16659; M01D:91252221
 A:Accession: S16661
 A:Molecule type: genomic RNA
 A:Residues: 1-377 <KAW2>
 A:Cross-references: EMBL:X57559; NID:961985; PID:CAA40740.1; PID:961986
 A:Experimental source: strain Joshua
 C:Genetics:
 A:Note: M
 C:Superfamily: parainfluenza virus matrix protein
 C:Keywords: matrix protein

Query Match 72.0%; Score 36; DB 1; Length 377;
 Best Local Similarity 60.0%; Pred. No. 20;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 PSAAVITVSP 10
 1 11111
 DB 170 PIVSITVSP 179

RESULT 9
 141257
 Hypothetical protein SP0285.11 - Hission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T41257
 R:Seeger, R.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrett, R.A.
 Submitted to the EMBL Data Library: September 1998
 A:Reference number: Z21981
 A:Accession: T41257
 A:Status: preliminary; translated from GH/EMBL/M084
 A:Molecule type: DNA
 A:Residues: 1-427 <SEE>
 A:Cross-references: EMBL:AF031545; PID:CAA20850.1; GSPDB:GN00068; S166:SNV285.11
 A:Experimental source: strain 972H-; cosmid c285
 C:Genetics:
 A:Gene: SP0B:SP0285.11
 A:Map position: 4
 A:Introns: 35/7

Query Match 72.0%; Score 36; DB 2; Length 427;
 Best Local Similarity 70.0%; Pred. No. 22;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 PSAAVITVSP 10
 1 11111
 DB 203 PSAAVITVSP 212

RESULT 10
 S62749
 Alpha X protein (alpha X) - braeker fungus (Schizophyllum commune)
 C:Species: Schizophyllum commune
 C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
 C:Accession: S62749
 R:Matillon, A.L.; Bartholomew, K.A.; Wu, J.; Yano, H.; Novotny, C.F.; Murray, R.J.
 Eur. J. Genet. 29, 143-149, 1996
 A:Title: The alpha mating type locus of Schizophyllum commune: structure and function
 A:Reference number: S62749; M01D:96418876
 A:Accession: S62749
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-537 <MAK>
 A:Cross-references: EMBL:U11943; NID:9327622; PID:AAA41399.1; PID:9327623
 A:Note: The nucleotide sequence was submitted to the EMBL Data Library: August 1994
 C:Genetics:
 A:Introns: 21/7
 C:Superfamily: Alpha X protein

Query Match 72.0%; Score 36; DB 2; Length 537;

A:Pathway: alcohol degradation
 C:Function: <RPH>
 A:Description: catalyzes the oxidation of retinol to retinal by NAD+
 A:Pathway: retinoic acid biosynthesis
 A:Note: retinoic acid regulates epithelial cell differentiation
 A:194: abundant in stomach, eye, skin, thymus, and ovary
 C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
 C:Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidoreductase
 F:2-374/Product: long-chain alcohol dehydrogenase homology <LADH>
 F:2-374/Product: alcohol dehydrogenase 7 *status experimental <MAT>
 F:12-365/Domains: long-chain alcohol dehydrogenase homology <LADH>
 F:194-223/Region: beta-alpha-beta NAD nucleotide-binding fold
 F:2/Modified site: acetylated amino end (Gly) (in mature form) *status predicted
 F:47-68-174/Binding site: zinc, catalytic (Cys, His, Cys) *status experimental
 F:98-101-104-112/Binding site: zinc, noncatalytic (Cys) *status experimental

Query Match 70.0% Score 45: DB 1: Length 474:
 Best Local Similarity 70.0% Pred. No. 41:
 Matches 7: Conservative 0: Mismatches 4: Indels 0: Gaps 0:

1 PSAAVATYSP 10
 111 111 1
 296 PSAAKMLTYP 305

RESULT 14

A56436
 A:alcohol dehydrogenase (EC 1.1.1.1) IV - mouse
 N:Alternate names: class IV alcohol dehydrogenase mu chain; class IV alcohol dehydrogenase
 N:Contains: retinol dehydrogenase (EC 1.1.1.105)
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Jul-1995 *sequence_revision 21 Jul-1995 *text change 11 Jun 1999
 C:Accession: A56436
 R:Zygmunt Knicht, M.: Ang, H.L.: Fodillo, M.H.: Dunstey, G.
 J. Biol. Chem. 270, 10868-10877, 1995
 A:Title: Cloning of the mouse class IV alcohol dehydrogenase (retinol dehydrogenase) cDN
 A:Reference number: A56436; MIM:95256259
 A:Accession: A56436
 A:Molecule type: mRNA
 A:Residues: 1-374 <230>
 A:Cross-references: GH:020257; NID:q897584; PUD:AAA76745.1; PII:q847985
 C:Genetics:
 A:Gene: Adh-3
 C:Complex: homodimer
 C:Function: <ADH>
 A:Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes an
 C:Function: <RPH>
 A:Pathway: alcohol degradation
 A:Description: catalyzes the oxidation of retinol to retinal by NAD+
 A:Pathway: retinoic acid biosynthesis
 A:Note: retinoic acid regulates epithelial cell differentiation
 A:Note: abundant in stomach, eye, skin, thymus, and ovary
 C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
 C:Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidore
 F:2-374/Product: long-chain alcohol dehydrogenase homology <LADH>
 F:12-365/Domains: long-chain alcohol dehydrogenase homology <LADH>
 F:194-223/Region: beta-alpha-beta NAD nucleotide-binding fold
 F:2/Modified site: acetylated amino end (Gly) (in mature form) *status predicted
 F:47-68-174/Binding site: zinc, catalytic (Cys, His, Cys) *status predicted
 F:98-101-104-112/Binding site: zinc, noncatalytic (Cys) *status predicted

Query Match 70.0% Score 45: DB 1: Length 474:
 Best Local Similarity 70.0% Pred. No. 41:
 Matches 7: Conservative 0: Mismatches 4: Indels 0: Gaps 0:

1 PSAAVATYSP 10
 111 111 1
 296 PSAAKMLTYP 305

RESULT 15

133663

Hypothetical protein W0485.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 *sequence_revision 29-Oct-1999 *text change 29-Oct-1999

C:Accession: U4664

R:Smith, A.: Gibson, A.

submitted to the EMBL Data Library, October 1998

A:Description: the sequence of C. elegans cosmid W0485.

A:Reference number: Z21485

A:Accession: U4664

A:Status: preliminary; translated from GH/EMBL/DBL

A:Molecule type: DNA

A:Residues: 1-424 <SM1>

A:Cross-references: EMBL:AF100305; PUD:MAC68946.1; GSPDB:CM00021; GSP:W0485.3

A:Experimental source: strain Bristol N2; clone W0485

C:Genetics:

A:Gene: GSP:W0485.3

A:Map position: 4

A:Features: 7/3; 6/3; 102/3; 124/3; 144/3; 198/3; 277/3; 301/3; 417/3; 433/3

Search completed: March 12, 2002, 12:49:02
 Job time: 267 sec

Query Match 70.0% Score 45: DB 2: Length 424:
 Best Local Similarity 70.0% Pred. No. 45:
 Matches 6: Conservative 4: Mismatches 1: Indels 0: Gaps 0:

1 PSAAVATYSP 10
 111 111 1
 282 PSAAVATYSP 291

Tue Mar 12 14:28:00 2002

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